OM_of: US-09-525-998A-11 to PIR_68 * optimal   pfs

Date: Apr 23, 2002 10:12 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL-frame_n2p.model -DEV-xlp
-C-rpr_1 -inp1-Sprot-ss-1.pir -inp2-us-09-525-998a-11.txt -query-1 -subject-qpi-query fasta_1 2000
-DB-PIR_68 -OFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT-4.000
-MINMATCH-0.100 -Lqopt=0.000 -Lqopt=0.000 -q=GAPop-4.500
-QGAPEXT-0.050 -XGAPop-10.000 -X:GAPEXT-0.500 -FGAPop-6.000
-FGAPEXT-7.000 -YGAPop-10.000 -Y:GAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-opt -THR_MAX-100 -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-20000000000 -USER-USU4-MCEN1_1_94 -NCPU-6 -ICPU-3
-LONGLOG-NO_XLPXY -WAIT -THREADS-1

Search information block:
Query: US-09-525-998a-11
Query length: 600
Database: PIR_68:*
Database sequences: 219241
Database length: 76174552
Search time (sec): 113.890000

score_list:
Sequence	Strd Orig	ZScore	EScore	Len	Documentation
pir1:QHHUT1	1117.50 1650.46	1 3e-84	455	tumor necrosis factor receptor
pir2:JC4302	822.09 1211.96	3.5e 60	461	tumor necrosis factor receptor
pir1:GGMSU1	787.00 1141.49	2.7e-57	454	tumor necrosis factor receptor
pir1:GQRTT1	774.50 1141.49	3.0e-56	461	tumor necrosis factor receptor
pir2:S54182	213.50 309.57	6.8e-10	435	tumor necrosis factor receptor
pir1:QQHUTN	207.50 300.04	2.1e-09	427	nerve growth factor receptor pr
pir1:A26431	192.50 280.06	2.1e-08	425	nerve growth factor receptor pr
pir1:H43692	190.50 277.41	1.6e-08	325	t2 protein - rabbit fibroblast vir
pir1:GcV2M1	187.50 272.42	1.0e-07	324	t2 protein - myxoma virus (stra
pir2:B38644	181.00 260.77	3.9e-07	474	tumor necrosis factor receptor
pir2:I48854	176.00 253.57	2.6e-07	459	gene murine tumour necrosis fac
pir2:A46476	170.50 248.20	6e-06	405	R cell-associated surface mole
pir2:A46484	169.50 246.24	3.1e-06	327	apoptosis-mediating membrane as
pir2:I92175	166.50 241.31	4.6e-06	349	G2R protein - variola minor vir
pir2:T29623	164.00 237.65	8.2e-06	348	hypothetical protein G2R - vari
pir2:D36858	164.00 237.63	8.7e-06	349	gene G4P protein - variola vir
pir1:A35356	162.50 233.51	1.1e 05	461	tumor necrosis factor receptor
pir1:A49055	154.50 225.82	5.5e-05	460	C2Y antigen precursor - mouse
pir2:C12125	154.00 219.28	5.3e-05	277	trophoblast/lymphocyte surf
pir2:A46517	150.00 218.87	0.0001	260	C227 antigen precursor - human
pir2:JC2396	149.00 215.84	0.0001	324	Fas antigen precursor - rat
pir1:IN0006	148.00 212.79	0.0002	416	nerve growth factor receptor 1
pir2:A60771	146.50 212.58	0.0003	1680	R-cell activation protein CD40
pir2:A43434	143.50 196.49	0.0004	272	turin (EC 3.4.21.75) 2 - trait
pir2:I18700	137.50 236.02	0.0014	314	gene ox40 protein - mouse
pir2:I37383	134.00 193.85	0.0022	314	FAS soluble protein - human
pir2:S4583	134.00 192.46	0.0022	1548	serine proteinase (EC 3.4.21.
pir2:602428	133.00 185.18	0.0028	899	subtilisin-like preprotein conv
pir2:C6149	132.00 185.00	0.0028	415	subtilisin-like preprotein co
pir2:S12783	131.50 191.14	0.0043	271	OX40 antigen precursor - rat
pir2:A42086	131.00 185.03	0.0043	595	CD30 antigen precursor - human
pir2:A10636	130.50 188.21	0.0051	335	apoptosis-mediating surface ant
pir2:T23433	127.00 165.68	0.0074	3672	hypothetical protein K8C7.3
pir2:T37316	127.00 166.52	0.0074	3704	probable lamnin alpha chain
pir2:T37552	125.00 177.32	0.0124	557	'variant-specific surface protei
pir2:I37552	124.50 180.61	0.0164	277	OX40 homolog human
pir2:T31070	124.50 165.51	0.0124	192	notch homolog sea urchin (Ly
pir2:T25513	123.00 180.88	0.0228	192	hypothetical protein 20146.13
pir2:T27283	123.00 176.30	0.0128	1620	hypothetical protein YAC2CA.2
pir2:A48820	121.50 170.30	0.0233	728	probable transcription regulato
pir2:T43251	121.50 165.61	0.0239	1200	turin (EC 3.4.21.75), full a

seq_documentation_block:

seq_name: pir1:GHUT1

tumor necrosis factor receptor 1 precursor [validated] - human
A:Alt_names:tumor necrosis factor receptor type 1, TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitory tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Feb-2000
R:Accession: A48208; A34606; A44606; A44606; A48208; A48208; S12007; JI9758; A62231;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRI) and localization to
A:Reference number: A19298; MUID:92250049
A:Accession: A48208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g143748; PIDN:AAA61201.1; PI
Rioetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesss
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A48899; MUID:90245284
A:Accession: A48899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M54286; GB:M33480; NID:g143753; PIDN:AAA47754.1; PID:g143754
A:Experimental source: placenta
A:Note: part of this sequence, including the amino end of the mature protein, confim
P:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A4900; MUID:90245285
A:Accession: A4900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M63121; NID:g143751; PIDN:AAA61761; PID:g143745
H:Himmler, A.; Maurer-Fogy, I.; ...
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A4555; MUID:91090841
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g143755; PIDN:AAA61764.1; PID:g143756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 1-455 <HIM>
A:Note: the modified protein, called tumor necrosis factor binding protein, is a solu
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A29281; MUID:91017503
A:Accession: A48281
A:Molecule type: mRNA
A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
R:Nphar, Y.; Kemper, D.; Blakebrough, R.C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtm
FMBO J. 9, 3269-3278, 1990
A:Note: Soluble forms of tumor necrosis factor receptors (TNF-bp), the cDNA for the
te form of the receptor.
A:Reference number: S12007; MUID:92060421
A:Accession: S12007
A:Molecule type: mRNA
A:Residues: 1-455 <NHP>
A:Cross-references: MUID:XXXXX; NID:g143754; PID:XXXX.1; JIB:g143724
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993

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Align seg 1/1 to GGHUT1 from: 1  to: 455

  1 ATGGCCTCCACCAGGCTGTGCCTGTCCTGCTGGTGCTCTGGA  50
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  1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl  17

 51 GCTGTGGTGGGAATATACCCCTCAGGGTTATTGGA............  87
    |||||||||||||||||||||||||||||||
 17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL  34

 88 ..........GATACGTGTGCTCCCCAAGGAAAATATATC 117
              |||||||||||||||||||||||||||||||||||
 34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle  50

118 CAGCCTAAAATAATTGATTGCATGCATGACAAAGAAGATA 167
    |||||||||||||||||||||||||||||||||||||||||
 51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  67

168 CTTCACAAGACTGTCCAGGCCTGCGGAGGATACCGACTCCAGGCAGT 217
    |||||||||||||||||||||||||||||||||||||||||||||||
 67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  84

218 GTGAGAGCGGGACCTTCACCGCTTCAAAAAGCATCACAGACACTGTGTC 267
    ||||||||||||||||||||||||||||||||||||||||||||||||
 84 ysGluSerGlySerProThrAlaSerGluAsnHisLeuArgHisCysSerLeu  100

268 ACTGTCTGCAAATGGGAAAGGAAATGGTGCAGGAGGAGATCCTGTCTG 317
    ||||||||||||||||||||||||||||||||||||||||||||||||
101 SerCysSerLysCysSerArgLysGluMetGlyGlnValGluLeuSerSerCy  117

318 CACAGTGGACTGGACAGCTGTGGGTGTCTGGAAGAAGAACCAGTAACGGC 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||
117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH  134

368 ATTATTGGACTGAAAACCTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
    |||||||||||||||||||||||||||||||||||||||||||||||||
134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  150

418 AATGGAACTGTAACTTCTGTGGAAGAAAAGAAAACAAGGTGACA 467
    |||||||||||||||||||||||||||||||||||||||||||
151 AsnGlyThrValHisLeuSerCysSerGlnAsnGlyLysAsnThrValCysTh  167

468 CTGCCATGCAGTGTTCCTGCTTGCAAGCTGCTCCTCCCCACTA 517
    |||||||||||||||||||||||||||||||||||||||||||
167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA  184

518 ACTGTAAGAAGAGCCTGGAGTGCACAAAGTTGTGCCTACCCCAGATTGAG 567
    ||||||||||||||||||||||||||||||||||||||||||||||||||
184 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu  200

568 AATGTAAAGAACAT AGAAAACACA 600
    ||||||||||||||||||||||||
201 AsnValLysAsnIleGluAsnThrThr  211
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seq_documentation_block:

A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758, MUID:94085779
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol 20, 1167-1174, 1990

A;Title: tumor necrosis factor inhibitor. purification, NH-2 terminal amino acid sequen
A;Reference number: A60231; MUID:90292116
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Lc
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
lieds.
A;Reference number: A38258; MUID:91062364
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G
Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
A;Reference number: A60594; MUID:89171156
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XF',66,'FIS
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-184,'X',188-201 <KA'>
A;Experimental source: urine
C;Comment: This protein is composed of two known receptors for both TNF-alpha (cachectin) and
C;Genetics:
A;Gene: GDB:INFR1
A;Cross-reference: GDB:125513; OMIM:191190
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol Biochem 58, 2264-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A;Reference number: JC2404; MUID:95128033
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-184,'X',188-201 <KA'>
A;Experimental source: urine
C;Comment: extracellular #status predicted .EXT.
F;1-21/Domain: signal sequence #status predicted .SIG
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted .EXT.
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-211/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted .MEM.
F;235-455/Domain: intracellular #status predicted .INT.
F;54-145,157/Binding site: carbohydrate (Asn) (covalen) #status predicted
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                Quality:  1117.50    Length:    211
                Ratio:    5.588      Gaps:        1
Percent Similarity:  94.787    Percent Identity:  94.787

alignment_block:
US-09-525-998A-11 x GGHUT1
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Right column reference block:

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seq_name: PIR2:JC4302

seq_documentation_block:

A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-451 <SUT>
A;Cross-reference: GB:U04904; NID:g1141752; PID:AAC48499 1; PID:g1141753
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 17 <SU2>
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24 Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 264-266, 1995
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A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology
C;Keywords: glycoprotein, kidney, receptor, transmembrane protein, tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;41-82/Domain: NGF receptor repeat homology <NGF>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIG>
F;54,145,151/Binding site, carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
                Quality: 822.00   Length: 211
                Ratio: 4.670   Gaps: 2
Percent Similarity: 83.412   Percent Identity: 69.668

alignment_block
US-09-525-998A-11 x JC4302

Align seq 1/1 to: JC4302 from: 1 to: 461

    1 ATGGCCCTCCACCGGTTCAGTGTGATCTTCTTGGA 50
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    1 MetGlyLeuSerThrValProCysLeuCysProLeuValSerLeuArgAl 17

   51 GCTGTTGTTGGGAAGAATAT...CTAGGGCATATTGGA   87
      ||||||||||| ||| |||
   17 aLeuLeuValAspValTyrProAlaGlyValHisGlyLeuValLeuHisP 34

   88 .... GATAGTGTGTGTGCTCCTCAAGGAAAAATATATT 117
                  |||||||||||||||||||||||||||||||||
   34 roGlyAspArgValLysArgGluSerProGlyLeuTyrCysProGlyGlyLeuTyrTyrSer 50

  118 CACCCTCAAAAATAATTGATTTGTGTACCAAGTGCCACAAAGGAACCTA 167
      ||||||||||||||||||||||||||||||||||||||||||||||||
   51 HisProGlnAsnArgSerIleCysCysThrLysCysHisLysGlyThrTy 67

  168 CTTGTAAAATGAGTGTGGCCGAGAGGATAGAGATGATCAGGAGT 217
      |||||||||| ||||||||||||||||||||||||||||
   67 rLeuHisAsnAspCysSerLeuTyrProGlyLeuAspAspThrAspCysSerArgGlu 84

  218 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 267
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   84 rSerAspAsnGlyThrPheThrAlaSerGluAsnHisLeuThrGlnCysSerLeu 100

  268 AGCTCCTCCAAATGGGAAAGGAAATGGTCAGTGGAGATCTCTTCTTG 317
      ||||||||||||||||||||||||||||||||||||||||||||||||
  101 SerCysSerCysLysCysSerArgSerGlnMetSerGlnValGluIleSerProProCy 117

  318 CATAGTGGATATGGGATGTGTGGTGGTATAGGAAGAAATCTAGTAGGGT 367
      ||||||||||||||||||||||||||||||||||||||||||||||||
  117 sThrValAspArgAspThrCysValCysSerGlyTyrGlyLysLysAspGlyTyrArgArgL 134

  368 ATTATTGCAGGAAAACTTTTCCAGGTGCCTGCCTGCC 417
      |||||||||||||||||||||||||||||||||||||
  134 ysTyrTrpSerGluThrLeuProPheGlnCysLeuAsnCysSerLeuCysSerPro 150

  418 AATGGAGACCCTCACCTGCACAGAGAAAAAAGAGCATAA 467
      |||||||||||||||||||||||||||||||||||||||
  151 AsnGlyThrValGlnLeuProCysSerLeuGluLysGlnAspAsnThrIleCysAs 167

  468 CTGGCATGGACGTTCTTCAAGAAAAGATGTCTTCTGGATA 517
      ||||||||||||||||||||||||||||||||||||||||
  167 nCysHisSerGlyGlyPhePheArgAspLysLysCysValSerCysValA 184

  518 ACAGGAAGAAAAGGCTGGAACCACCAAGCGTGGCTAGCAGGAAG 567
      ||||||||||||||||||||||||||||||||||||||||||||
  184 snCysLysAsnAla AspCysLysAsnLeuCysProAlaThrSerGln 199

  568 AATGTTAAGGCACTGAGGACTCAGGACCACA 600
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  200 ThrArgAsnAspPheGlnAspProArgThrThr 210

seq_name: piri:GQMST1

seq_documentation_block:
   tumor necrosis factor receptor 1 precursor - mouse
   N;Alternate names: tumor necrosis factor receptor p55
   C;Species: Mus musculus (house mouse)
   C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Dec-2000
   C;Accession: A38634; I48254; S16677; S19026; JC4302; JQ0926
   R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
   Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
   A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
   A;Reference number: A38634; MUID:91187885
   A;Accession: A38634
   A;Molecule type: mRNA
   A;Residues: 1-454 <LEN>
   A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39825; PID:g199826
   R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
   Mol. Cell. Biol. 11, 3020-3026, 1991
   A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
   A;Reference number: A40254; MUID:91246168
   A;Accession: B40254
   A;Molecule type: mRNA
   A;Residues: 1-454 <COD>
   R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fel
   Eur. J. Immunol. 21, 1649-1656, 1991
   A;Title: Cloning, expression and cross linking analysis of the murine p55 tumor necro
   A;Reference number: S16677; MUID:91285014
   A;Accession: S16677
   A;Molecule type: mRNA
   A;Residues: 1-454 <HAR>
   A;Cross-references: EMBL:X59328; NID:g15978; PIDN:CAA41922.1; PID:g54579
   R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   Immunogenetics 34, 338-340, 1991
   A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
   A;Reference number: S19021; MUID:92039815
   A;Accession: S19021
   A;Molecule type: mRNA
   A;Residues: 1-454 <ROT>
   A;Cross-references: EMBL:X67799; NID:g54848; PIDN:CAA40936.1; PID:g54849
   R;Bebo, B.F.;
   Immunogenetics 39, 450-451, 1994
   A;Title: Nucleotide sequence of the TNF type 1 receptor from a mouse endothelioma cel
   A;Reference number: 154532; MUID:94245292
   A;Accession: 154532
   A;Status: translated from GB/EMBL/DDBJ
   A;Molecule type: mRNA
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   A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA53361.1; PID:g430733
   R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
   Mol. Immunol. 30, 165-176, 1993
   A;Title: Genomic organization, cellular #status predicted #status predicted #status
   A;Reference number: 157826; MUID:93156721
   A;Accession: 157826
   A;Molecule type: DNA
   A;Residues: 1-393 <RES> 395-454 <RES>
   A;Cross-references: GB:M75156; NID:g202100; PIDN:AAA40445.1; PID:g202102
   C;Comment: this protein is one of two distantly related receptors for both TNF-alpha
   C;Genetics: TNFR-2
   A;Genc: TNFR-2
   A;Interval: 1-454 in DNA
   C;Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology
   C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane pro
   F;1-29/Domain: signal sequence #status predicted <SIG>
   F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
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   F;44-82/Domain: NGF receptor repeat homology <NGL>
   F;84-126/Domain: NGF receptor repeat homology <NGL>

F:127-167/Domain. NGF receptor repeat homology <N3>
F:168-204/Domain. NGF receptor repeat homology <N4>
F:214-234/Domain. transmembrane #status predicted <MEM>
F:235-454/Domain. intracellular #status predicted <INT>
F:54,151,201/Binding site. carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
　Quality:　787.00　　　　　　Length:　211
　Ratio:　4.523　　　　　　　　Gaps:　2
Percent Similarity:　82.464　　Percent identity:　66.351

alignment_block
US-09-525-998A-11 x GQMSI1

Align seg 1/1 to: GQMSI1 from: 1 to: 454

　　1 ATGGGCTCGCTCCTGCCGCTGCTGCTGCTCCTGCTGCTGCTCCTGGA 50
　　　 ||||||||| ||||||| ||||||||||| |||||||||
　　1 MetGlyLeuThrValProGlyLeuLeuLeuLeuSerLeuValLeuAcuA1 17

　51 GCTGTTGGTGGAATATACCCCTCAGGGTTATTGGA 87
　　　 ||||||||||:::|||||||||| ||
　17 aLeuLeuMetGly?leHisProSerGlyValThrGlyLeuValProSerL 34

　88 .............................GATAGTGTGTCCCCAAGGAAAATATATC 117
　　　　　　　　　　　　　　　　　　　　　　　||||||||||||
　34 euGlyAspArg?::;sA:?A(?::?::?,sFic:?:;GGl;?;sTrpVal 50

118 CACCCTCAAAATAATTCGATTCGCTACCAAGTGCCACAAAGGAACCTA 167
　　　 ||||||| ||||||||||||||||||||||||||||
　51 HisSerLysAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

168 CTTGTAAAGGATGTCAAGGCGAGGACGATATCGATAGATCGATAGGGAGT 217
　　　 :||||||| |||:||| ||||| ||||||||
　67 rLeuValSerAspCysProSerProGlyArgAspThrValCysArgGluC 84

218 GTGCAGAGCGGCTGCCTCACCGACAGAAAACCACCCAGACACTGCCTC 267
　　　 :||:||||||||||||||||||||||:|||||||| ||||||||
　84 ?sGluL;sGlyThrPheThrAlaSer?:AsnCysGlnCysGlnCysLeu 100

268 AGCTTGCTGCAAATGCCCAAAGAAATGGTCAGGTGGAGATCTCTTCTG 317
　　　 ||||||::: ||||||| ||||||||||||||
101 SerCysLysThrCysArgLysGluMetSerGlnValGluIleSerProCy 117

318 TACAGTGACCGGAGCACCGTGTGTGTCGAGGAAGAACCAGTACCGGC 367
　　　 |||||||||||||:|||||||||| |||||||||
117 sGlnAlaAspLysAspThrValCysGlyCysLysCysGluHisCcCcA 134

368 ATTATTGGAGTCAAAAACCTTTCTAAGAAAAGAGTGTGTCTCCTGTAGTA 417
　　　 :|||||||||||||:::||||||||||||||||||||
134 rqTyrLeuSerGluThrGlnHisPheThrAlaSerGlnClnserGlnSerH 150

418 AATGGGACCGGTGCACCCTCTCTCCCCCAGGAGAAACAGACAGCGGTGGCAC 467
　　　 |||||||||||||||||:::|||||||||||||||||||
151 AsnGlyThrValThr?lieProCysLysGlyGlnAspThrValCysAs 167

468 CTGCCATGCAGGTTCTTCTAGAGAAAGAGTGTGTCTCTGTAGTA 517
　　　 :||||||||||:::||||||||||||||
167 ?CysHisAlaGlyPhePhoLeuArgGluSerGluCysValProCysSerH 184

518 ACTGCAACAAAACCCTCGCAGCTGCACCAAGCTGTGCCTA...CCCCAGATT 564
　　　 ||||||||:::||||||||||||||||||||||
184 isCysLysLysAsnGluGlyCysSMetCysLccCysLeuProProProLeu 200

565 GAGAATGCTAAGGCGCACTCAGGCACTCAGGCACC 597
　　　 ||||||||:::||||||||||
201 AlaAsnValThrAspProGlnAspProSerGlyThr 211

seq_name: pir1:GQRTT1

seq_documentation_block:
tumor necrosis factor receptor 1 precursor - rat

N:Contains tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 67 xxx 1994 #text_change 22-Jun-1999
C:Accession: B36555
R:Himmler, A.; Maurer Fogy, I.; Kroenke, M.; Scheirich, P.; Fliesenaier, K.; Loot; M.
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555, MUID 91090841
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <HIM>
A:Cross-references: GB:M63122; NID:g207361; PIDN:AAA12256.1; PID:g207342
C:Comment: this protein is one of two known receptors for both TNF alpha (cachectin)
C:Superfamily. tumor necrosis factor receptor type 1, NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain. signal sequence #status predicted <SIG>
F:30-461/Product. tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain. extracellular #status predicted <EXT>
F:30-201/Product. tumor necrosis factor binding protein #status predicted <IHP>
F:44-82/Domain. NGF receptor repeat homology <NC1>
F:84-126/Domain. NGF receptor repeat homology <NC2>
F:127-167/Domain. NGF receptor repeat homology <N63>
F:168-204/Domain. NGF receptor repeat homology <N64>
F:212-234/Domain. transmembrane #status predicted <MEM>
F:235-461/Domain. intracellular #status predicted <INT>
F:54,151,201/Binding site. carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
　Quality:　774.50　　　　　　Length:　210
　Ratio:　4.583　　　　　　　　Gaps:　1
Percent Similarity:　89.476　　Percent identity: 64.762

alignment_block
US-09-525-998A-11 x GQRTT1

Align seg 1/1 to: GQRTT1 from: 1 to: 461

　　1 ATGGGCTCGCTCCTGCCGCTGCTGCTGCTCCTGCTGCTGCTCCTGGA 50
　　　 |||||||| |||||||| |||||||| ||||||||||||||
　　1 MetGlyLeuProlleValProGlyLeuLeuSerLeuValLeuLeuLeuAl 17

　51 GCTGTTGGTGGAATAGACCCCTCAGGGTTATTGGA 87
　　　 |||||||||:::|||||||||||||||||||
　17 aLeuLeuMetGlyIleHisProSerGlyValThrGlyLeuValProSerL 34

　88 　　　　　　　　　　　GATAGTGTGTCCCCAAGGAAAATATATC 117
　　　　　　　　　　　　　　||||||||||||||||||
　34 euGlyAspArgGluLysArgAspAsnLeuCysProLeuGlyLysAlaYrAla 50

118 CACCCTCAAAATAATTCGATTGTGTACCAAGTGCCACAAAGGAACCTA 167
　　　 |||||:::|||||||||||||||||||||||||||||||||||
　51 HisProLysAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

168 CTTGTAAAGGATTGTGAAGGCGAGGATATGGATAGATCGATAGGGAGT 217
　　　 ||||||| |||||||||||||||||||||||||
　67 rLeuValSerAspCysProSerProGlyArgAspThrValCysArgGluC 84

218 GTGCAGAGCGGCTGCCTCACCGACAGAAAACCACCCAGACACTGCCTC 267
　　　 |||:||||||||||||||||||||||:|||||||| ||||||||
　84 ysGluLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeu 100

268 AGTTGCTCAAATGCCCAAAGGAAATGGGAGGAAAATGGTCAGGATCTCTTCTG 317
　　　 ||||||::: |||||||||||||||||||||| ||
101 SerCysLysThrCysArgLysGluMetPheGlnValGluIleSerProCy 117

318 CACAGTGACCGGAGCACCGTGTGTGGCGAGGAAGAACCAGTACCGGC 367
　　　 |||||||||||||:::||||||| |||||||||
117 sLysAlaAspMetLysAspThrValCysGlyCysLysLysAsnGlnPheGlnA 134

368 ATTATTGGAGTCAAAAACCTTTCCAGTGGTTTCAATTGCAGCCTCTGCCTC 417
　　　 :|||||||||||||:::||||||||||||||||||||
134 rqTyrLeuSerGluThrHisProAsnGluThrAlaSerCysThrProCysPhe 150

```
418  AATGGGACCCTGTATTCTCTGTAGGATAAA·AAA·AAAA·AAA·ACGGTGGAC 467
     ||||||||||     :::  ||||   |||||               ||:|||
151  AsnGlyThrValThrLeuProCysLysGluLysGlnAsnThrValCysAsAs 167

468  CTGCCATGCAGTCTTCTTTCTAAGAGAAACGATGTGTCTCGTGTAGTA 517
     :||||||| |  |||||||    |||||||||||   |||||:|:|||
167  nCysHisAlaGlyPhePheLeuSerGlyAsnGlyLysThrProCysSerH 184

518  ACTGTAAGAAAAGCCTGGACTGCACGAAGTGTGCCTACCCCAGATTGAG 567
     ||||||||:  |||||| |||   |||||||||||||||||||
184  isCysLysLysSerLeuGluCysThrLysCysAlaTyrProArgProValAla 200

568  AATGTTAAGGGCACTGAGGACTAGGCACC 597
     |||||     ||||||||||||||
201  AsnValThrAsnProGlnArgProSerGlyThr 210
```

seq_name: pir2:154182

seq_documentation_block:
tumor necrosis factor receptor 2 related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17 Mar 2000
C:Accession: 154182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: 154182; MUID:93252381
A:Accession: 154182
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04276; MUID:g347761; PIDN:AAA36757 1, PIDg347762
C:Genetics:
A:Gene: GDB:THR
A:Cross-references: GDB:1230195; OMIM:600079
A:Map position: 12p13 1-12p13 1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

alignment_scores:
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         Quality:  213.50            Length:  214
         Ratio:    1.923             Gaps:    11
Percent Similarity: 51.860   Percent Identity: 30.841
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alignment_block:
US-09-525-998a-11 x 154182

Align seq 1/1 to: 154182 from: 1 to: 435

```
33   GCCACCTGCTGCTGCGGGAGGTGTTGGTGGGAAAATAAACCCTGGAGGGGTTA  82
     ||||||||      :::  ||||   ||| |||    ||
6    AlaThrSerAlaProGly.......AlaArgCys.ProLeuValLeu.GlyLeuP 22

83   TTGGA........                                          87
     ||||||
22   heGlyLeuLeuAlaAlaSerCInProGlnAlaVaIProProTyrAlaSer 38

88   ...GATAGTGTGCT........GGCCAAGGAGAAAAATATCCACCCTCAAAA 128
     |||||     :::   ||||||    |||    |||
39   GluAsnGlnThrCysArgAsp......GlyLysTyrThrGluProGlnHis 55

129  TAATTCGATTTGCTGCACCACCAAGCAGCACAAACGAACCTACTTCTACAATG 178
     ||||     :::  ||||||    ||    :::   |||    |||
55   sArg....IleCysThrCysSerArgCysProSerGlyThrTyrValSerAlaAl 71

179  ACTGTCTGGGGGGA·GGTAAAA·GGA·TGTA·GTA·AGTGTGTAGGGCGGC 228
     ||||     ||||||    |||   :::   |||    |||
71   ysCys...SerArgIleArgAspThrValCysAlaThrCysAlaGluAsn 86

229  TCTTCACCCCTCACAAAAAACCACGACACTCCTCACGCCCGCCAA 278
     |||||     |||  ||||   :::   ||||    |||
87   SerTyrAsnGluHisTrpAsnTyrLeuThrIleCysGlnLeuCysArgPr 103
```

```
295  ATGGGAAAA·AAAA·GG·CAGGGGAGAG·GGGTGGA·AGGATTG·AAA·AAGA 328
     |||     :::   ||||   |||    :::   ||||
103  oCysAspAlaProValMetGlyTyrLeuCysThrTyrCysAlaProGlyThrTyr 120

329  GGGACAACGTGGTCTGGTCGACGAGAAAAAAGAGTACAGATTATTGGAGT 378
     ||     :::   ||||   |||    :::   ||||
120  ValLeuGlySerAspGluThrArgGlnAspThrLysMetPro...AlaCysA 136

379  GAAAACCTTTCCAGGCTTCAATTGCAGCCTC.........TGCCTCCAA 419
     ||     :::   ||||   |||    :::
137  ..LysGluLeuGluGlnCysThrHisCysSerLeuLeuSerArgAspCysProPr 154

429  TGGGAA·GGA·AGGTAGGGGA·AAA·A......AAA·AAA·AAAAGGT 464
     ||     :::   ||||   |||    :::
150  oGlyThrGlnAlaAspLysCysAspAsnGlyValGlyTyrTyrAsnAsnHisG 167

464  GCACC......AGA·AGGTTC·ITC·IAA·AAAAA·AGGGGATCC 510
     ||     :::   ||||   |||
167  ysValProCysLysAsnGlyHisPhe.....GlnAsnThrSer.ArgPro 181

511  IGTAGGAACIGTAAAAAACCTGGAGTGCACGAAGTGTGCCTACCCCA 560
     ||     :::   ||||   |||
182  SerAlaArgCysGluProHisThrArgCysGluAsnGlyHisLeu... 194

561  GATTGAAAATGTTAAAGGCTGAAGGACTAGGGACCACACA 600
     ||     :::   ||||
197  .ValGluAlaAlaProGlyThrAlaGlnSerAspThrHr 209
```

seq_name: pir1:QHDN

seq_documentation_block:
nerve growth factor receptor precursor, low affinity [validated] - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31 Mar 1988 #text_change 08 Dec 2000
C:Accession: A25218; A60204; S21889; I57638
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218. MUID:87055725
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <TGH>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AAH59544 1; PIDg189205
R:Marano, N.; Dietzschold, H.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob,
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth
A:Reference number: A60204; MUID:87065574
A:Accession: A60204
A:Molecule type: protein
A:Residues: 24-31, 33-42, 44-46, 48-49, 51, 53-54, 56 MAR
A:Experimental source: melanoma cell line A875
A:Notes: this sequence was corrected by a peptide isolated to follow the nucle
R:Visvader, J.; Sassone-Corsi, P.; Verma, I.M.; Becker, J.; Kann, A.B.
Arch. Biochem. Biophys. 294, 244, 252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21889; MUID:92198017
A:Accession: S21889
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183 <VIS>
R:Schgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-4167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor recept
A:Reference number: I57638; MUID:89099503
A:Accession: I57638
A:Status: preliminary; translated from GB:EM82:2331
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AAH59544 1, PIDg189205
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all

C;Comment   this protein is thought to form a high affinity receptor when it associates w
C;Comment   this receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication, glycoprotein, heterodimer, monomer, phosphoprotein, receptor, t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;33-65/Domain: NGF receptor repeat homology <NG1>
F;67-68/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TPM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
    Quality: 207.50   Length: 194
    Ratio: 1.921   Caps: 12
Percent Similarity: 55.670   Percent Identity: 31.443

alignment_block:
US-09-525-998A-11 x GQHUN

Align seq 1/1 to GQHUN from 1 to 427

  34 CCACTGGTGTGGCAGTGTTGGTGGTGGAAIAIACCTCAGGGTTAT   83
     :::|||| ||||||| ||||||| :::|||
  13 ProArgLeuLeuLeuLeuGlyLeuLeuGlyValSerLeuGlyGly....   27

  84 TGGAGATAGAGTGTGTGGCCAGGAAAGAAAAATATATGCACCCTCAAAATAATT 133
     ::: :::||||||||||| ||| ||| |||| ::: :||
  28 AlaLysGluAlaCysProSerThrGlyLeuTyrThrHis .... SerG 41

 134 GATTTGTGTACCAAGTGCCAAAAGAACCTACTTGTAAAAGACTGT 183
     :|||||| ||| |||||| ||||||||||||| ||
  41 GlyCysCysLysAlaCysAsn....GluGlyValAlaGluProCys 57

 184 CCAGGCCCGGAGAAGACTACTGCAGGAGCAGT   GAGAGAGGCTC 230
     || ||||||| ||| :::||| |||||||||||||
  58 ...GlyAlaAsnGlu....ThrValCysGluIleCysLeuAspAsnValIle 72

 231 CTTCACGGTTCAGAAAAACCATTCAGACACAGGTCCGGAGCGTGCCCGACCAAAT 280
     ||||| :::||| ||||| :::|||||| |||||||||||
  72 rPheSerAspValSerAlaThrGluProCysIysProCysThrGluC 89

 328 CGGCACACCGTCGTGCTGCGGGAAGAAGAACCAGTACCGGCACTATTGGGAG 377
     |||| ||||||| ||||||||||||||||| :::|||||||
 103 AspAspAlaValCysArgCys....AlaTyrGlyTyrTyrGlnAsnAs 116

 378 TGAAAAACCTTTCCAGTGGTTCCAATTGCCAGCGGCTCGGGCTTCAATTGGGACC 426
     ||:::   :::||| :::||||||||||||||||||||| :::
 116 pGluThrThrGlyArgCysGluAlaCysArgValCysGluAlaClySerG 133

 427 TTGGTAAGCTGCCTAGAAGAAGAAAGAAGACCTGGAGA   ANGTGC 471
     ::: ||| ||||||| :::|||||||||||||||||
 133 lyValGlyValPheSerGlnAsnGlnSerAsnThrValCysGluIysCys 149

 472 CATGCAGGTTTCTTGTAAGGAGAA   AAGGACAGCGGCTC 509
     ||| :::||||||| :::|||||| :::||
 150 ProAspGlyThrTyrSerAsp....AlaAsnHisValAsnProCysLeuPr 166

 510 CTGTAGTAACTGT   AATAAAAGGCTGCGAGCACAGCACCAGT 547
     ||::: ||| :::||||||||||||||

166 GCysThrValCysCluAspSerCysArgGlnLeuArgGlnCysThrArgt   183

548 TGTGCCTACCCAGATGACAGAATGGTTAAGGC   579

183 rpAlaAspAlaGluCysGluGluIleProGly   193

seq_name: pir1:A26431

seq_documentation_block:
nerve growth factor receptor precursor, low affinity   rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep 1999
C;Accession: A26431; PH1229
F;Radeke, M.T.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <PAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Meisis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retin
A;Reference number: PH1229; MUID:93077038
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C;Comment: The cysteine-rich region of the extracellular domain may form part or all
C;Comment: This protein is thought to form a high-affinity receptor when it associate
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication, glycoprotein, heterodimer, monomer, phosphoprotein; receptor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <EXT>
F;40-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-105/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:
    Quality: 194.50   Length: 192
    Ratio: 1.825   Gaps: 12
Percent Similarity: 55.208   Percent Identity: 50.208

alignment_block:
US-09-525-998A-11 x A26431

Align seq 1/1 to: A26431 from: 1 to: 425

  40 GTGCTCCTGGAGCTGTTGGGTGGTGGGAATAIATACCCTCAGGGGTTATTGGGAGA 89
     ||:::||| |||| |||||||||| :::|||||||||||||
  16 LeuLeuLeuLeuIleLeuGlyValSerSerGlyGly   .AlaLly 30

  90 TAGTGTGTGTCCCCAAGAAAAATATATCACCTCAAAATAATTCGATTT 139
     ||| :::||| |||||| ||| |||||||||||
  30 sGluthrCysSerThrGlyLeuTyrThrHis........SerGlyGluC 44

 140 GCTGTACCAAGTGCCACAAAGAAGACCTACTTGTACAAIGATGTGCCAGGC 189
     :::||| ||||||| |||||||||||||||| |||
  44 ysCysLysAlaCysAsnLeuGlyGluGlyValAlaGlnProCys...Gly 59

 190 CGGGGGCAGGATACGGCAGCGCAGGGAGCT   GAGAGCGGCTCCTTCAG 236
     :::||||||||||||||| |||||||||||

seq_name: pir2:B43692

seq_documentation_block:
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 10-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103
A:Accession: B43692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPI>
A:Cross-references: GB-M17433
C:Superfamily: myxoma virus T2 protein, NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NGR>
F:106-147/Domain: NGF receptor repeat homology <NGR>

alignment_scores:
Quality: 190.50   Length: 203
Ratio: 1.832   Gaps: 11
Percent Similarity: 51.232   Percent Identity: 29.044

alignment_block:
US-09-525-998A-11 x B43692

Align seq 1/1 to R43692 from 1 to 325

seq_name: pir1:G0V2ML

seq_documentation_block:
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macaulay, C.; StrReiher, M.; McFadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91385768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-426 <UPI>
A:Cross-references: A40566
C:Superfamily: myxoma virus T2 protein, NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NGR>
F:106-147/Domain: NGF receptor repeat homology <NGR>

alignment_scores:
Quality: 187.50   Length: 414
Ratio: 1.659   Gaps: 3
Percent Similarity: 48.707   Percent Identity: 25.000

alignment_block:

US-09-525-998A-11 x CQV2ML

Align seq 1/1 to CQV2ML from 1 to 326

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 40 GTGTCCTGAAGTGTTGGTGAAATATACCCTGAGGGTT               81
    ::|||||          ::||||         ::||::||
  6 loulqulaqAlalyrValaCysValTyrGlyGlyTAlaProTyrCl       22

 82 ATTGGAGATATGTGTGTCCCAAGAAAATATACCACCCTGAAATA       130
    :::||             |||          ::||:
 23 ..AlaAspArgGlyLysCysArgGlyAspGTyr.........GluLysA    36

131 ATTGGGATTTGCTGTGTAACCAAGCAGCCCAAAGGAACCTACTGTGACAATGAC 180
    :::||||||||||||||||||||  ||::|||||
 36 spGlyLeuCysCysTyrSerCysProGlySerTyrAlaSerArgLeu         52

181 TGTCCAGGCAGTCAGATGGATAGGAGAAGGACTC   240
    :| |||||||           ||::||||||::Th
 53 Cys...GlyProCysSerAspThrValCysSerllrCysllsAsnCysTh      68

231 CTTCACCGGTTCAAAAAACAACACTAGCCCCAGCTGC....TCCA          277
    ::||||||||  ||||     :::::|||||||
 68 rPheThrAlaSerThrAsnHisAlaProAlaCysValSerCysValArgGlyA   85

278 AATGGCCAAAGCAAAAGCCTCACCCTCCCACAACGGCCACACACCGGAC       327
    ::|||                        |||||
 85 SerCysThrGlyHisLeuSer........GluSerGlnSerCysAspLysThr   99

328 CGGGACACCGGTGTGGCTGGTGGAGGAAGAACCAGTAC                 363
    ||||| |||||   |||||||
100 ArgAspArgValCysAspCysSerAlaGlyAsnrfCysllcalleuCysGl     116

363                                                        363

116 yGlnGluGlyCysArgIleCysAlaProLysThrCysCysProAlaGlyT     133

363                                                        363

133 yrGlyValSerGlyHisThrArgThrsGlyAspValLeuCysThrCysCys    149

364 ..CGGATTATTGGATGGAAAACTTTTAAATTGTAGTTATTGGTTAATGGT     410
    :::||||          ::|||||||           ::||
150 ProArgTyrThrTyrSerAspAlaValSerSerThrGluThrCysThrSe     166

411 CTGGCCAATGGC   ACCTGTAACCTCTCTGGAGGAGAAAACGACA          457
    :||||||          :::||||         :::||||
166 rSerPheAsnTyrIlesSerValGluPheAsnLeuTyrProValAsnAspT    183

458 CGGTGGACACCGGCCATTGGCAGGTTTTTAAGAGAAAACGAGTGTGTC        507
    :|||||           ||||||||||         ||:||||
183 hrSerCysThrThrAlaGly.            ProAsnGluValVal        195

508 TCGTGTAGTAACTGTAACAAAGTTG      AGATTGACAAAGTT          548
    :::||             ||||||           :::||
196 LysThrSerGluPheSerVaTThrLeuAsnHisThrAspCysAspProVa     212

549 GTGGCTACCCCAGATTGCAGAATGTTAAGAGAACTACAGGATTGCAGGC       594
    ::||||           ::|||||         ::|||
212 lPheHisThrGluTyrrGlyTllySerGluGlyAlaGly                 227
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alignment_scores:

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        Quality:  181.00          Length:      161
          Ratio:    1.945           Gaps:        8
Percent Similarity:  57.764   Percent identity:  31.677
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alignment_block:
US-09-525-998A-11 x B38634

Align seq 1/1 to B38634 from 1 to 474

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 97 TGTGCCCAAGGAAAATATATCACCCTCAAAATAATTGGATTTGCTGTGTAC   146
    |||     :::|||||     ::::||||        :|||||||   :||
 49 CysGlnIleSerGlnGluThrTyrAspArgCysAlaGluMetCysCysCysAl  56

147 CAAGCGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGC   196
    :||||||     :::||||     :::|||||||        ||||||
 56 aLysCysProProGlyTyrGlnTyrValLysHisPheCys...AsnLysThrS  72

197 AGGATAACGGACTGCAGGAAGGTGAGAACAGCTCTTCCACCGGTTCAGAA   246
    ::||||||     |||         ::||||||||||        ||||||
 72 erAspThrValCysAlaAspCysGluAlaSerMetTyrThrGlnValTrp     88

247 AACCACTTCAGACTGACTGACGTGC     TCTAAAAGCCGAAAGGAAAT   293
    :::||||||           ||||||           ::::||||
 89 AsnGlnPheArgThrCysLeuSerCysSerSerCysThrThrAsp...      104

294 GGGTCAGGTGGAGACATCTTTGGCAGAGGAGGACAGGGACACGTGGTGTG   343
    ::||||||     :::|||||        ::::|||         :::||||
105     GlnValGluIleArgAlaCysThrLysGlnGluAsnArgValCysA    120

444 GTTGACAAGACACTAC                    CGGATATTGGACTGAA   381
    :||||||                                  ||||||||
120 laCysGluAlaGlyArgTyrCysAlaLouLysThrHis......SerGly    134

382 AAGCTTTCCAGTGCTGCAATTGTAGTTGGTTTAATGGT    ACCGT       428
    ||         :::|||||||        ::||||||           :::||
135 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVa    151

429 GCACCTCTCGGCCAGGAGAAAACAAAACACAGGC    ACCTGCCATG      475
    ::|||        :::|||||     ::||||           :::|||
151 lAlaSerSerArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaP     168

476 CAGGTTCTTTCTTCAAGAGAAAACGAGTGTGTCTCTGTGTAGTAACTGTAAG  525
    :||||          |||         ::|||||         ::||
168 rGlyThrPhe......SerAspThrSerSerThrAspValCysArg         182
```

526 AAAAGCCTGGAGTGCACGAAGTTGTGCCTAAGC 558
        ||||| |||::: |
183 ProHisArgIleCysSerIleLeuAlaIlePro 193

seq_name: pir2:I48854

seq_documentation_block:
B cell-associated surface molecule CD40, long splice form - mouse
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1994 #sequence_revision 02-Jul-1994 #text_change 23-Jul-1995
C:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848
A:Accession: I48854
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53091; PID:g433821
A:Cross references: EMBL:X76401; NID:g433830; PIDN:CAA53091; PID:g433821
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology <NGF>
F:151-188/Domain: NGF receptor repeat homology <NGF>

alignment_scores:
    Quality: 176.00   Length: 161
    Ratio: 1.913   Gaps: 8
Percent Similarity: 57.143   Percent Identity: 31.056

alignment_block:
US-09-525-998A-11 x I48854

Align seg 1/1 to: I48854   from: 1   to: 459

  97 TGTCCCAAGAAAATAIACAACCTCAAAAIAATTGCAITTGCTGTAC 146
       || |||| ||||:||||| ::::::||||||||: |
  25 CysGlnPheSerGlnAspTyrTyrAspArgLysAlaGlnMetCysCysAsAI 41

 147 CAAGIGCCACAAAGAAAGCTACTTGTACAAGAGTGGACCAGCCCGGAGGC 196
       ||||||||||| ||| | :::: ::: ::::::|||||||| |
  41 aLysCysProProGlyGlnTyrValLysHisPheCys....AsnLysThrS 57

 197 AGGAIAGGACTGCACGAGTGCAGTTCGAAGAGCTCCTCAGCTGTCAGAA 246
       :||||||| ||| ::||||||||||:|:|:|:| |||||| |
  57 crAspThrValCysAlaAspCysAlaSerMetTyrThrGlnValTrp 73

 247 AACCAGCTCACAACATGCCTAGTGC...TCCAAATGCGGAAAGGAAAT 293
       ||||||||| ||||||||||| ||:::|| ||: :::
  74 AsnGlnPheArgThrCysLeuSerCysSerSerCysThrAsp.. 89

 294 GGGTCAGGTCGCAGAGCTCTTCTTCACAGCTGGACACCGGGGTGTG 343
       |||||||||||||| : |||||| : |||||
  90 ...GlnValGluThrAlaCysThrLysGlnGlnAsnArgValCysA 105

 344 GCTGCAGAGAAATAGTAC   GGGCATTAITGGAGTGAA 381
       ||||||||||||||||| || |||||||||||
 105 laCysGluAlaGlyArgTyrCysAlaGluCysThrHis.....SerGly 119

 382 AACCTTTTCAGGCTTCAATTGAGCTCCTGCCTCAAIGGG...ACGGT 428
       ||||||| |||| |||| || |||||||||||| ||||| |||
 120 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVa 136

 429 GCACCTCTCCTGCGGCAGGAAGAAAAGGGACCGGTGCC...ACCTGCCATG 475
       ||||||||||||| |||| |||||||||||:| ||||||||||
 136 lAlaSerSerArgArThrArgAcAsnValArgCysLysAlaCysAlaF 153

 476 CAGGTTCTTTTCTTAAGAGAAAACGATGTGTCTCCTGTAGTAACTGTAAG 525
       ||| ||| ||: | | :|| || ||| ||||||||||||||||
 153 roGlyThrPhe.....SerAspThrThrSerSerThrAspValCysArg 167

 526 AAAAGCCTGGAGTGCACGAAGTTGTGCCTAAGC 558
       ||||: ||||::: |
 526 AAAAGCCTGGAGTGCACGAAGTTGTGCCTACC 558
       ||||: ||||::: |

168 ProHisArgIleCysSerIleLeuAlaIlePro 178

seq_name: pir2:A46476

seq_documentation_block:
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1994 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J.Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mouse CD40.
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <RES>
A:Cross-references: GB:M83312; NID:g155058
A:Note: sequence extracted from NCBI backbone (N:NIP:47426, N:BB:37207)
A:Note: this translation is not annotated in Genbank entry MUSCD40A, release 111.0
R:Grimaldi, J.C.; Torres, R.; Clark, E.A.; Barclay, A.N.; Ward, M.; Gordon, J.
J.Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:94094586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287 <RES>
A:Cross-reference: GB:M83312; NID:g155058
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (N:NIP:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

alignment_scores:
    Quality: 170.50   Length: 148
    Ratio: 1.579   Gaps: 10
Percent Similarity: 57.447   Percent Identity: 28.191

alignment_block:
US-09-525-998A-11 x A46476

Align seg 1/1 to: A46476 from: 1 to: 305

  52 CTGTTGGTGGAAATATACCCCTCAGGAGTTATTGGAGATATGGTG...TG 98
       ||: |||||||||||||||| |||||| :|||||||||| |
  14 LeuLeuThrAlaValHis.................LeuGlyGlnCysValThrGly 26

  44 TGCCTAAGAAAATAAGACCCTGCAAATAATAGCCATTGCTGGCTGTGACCA 148
       |||||||||||||| ::: ||| |||| ||||||||||||||
  26 sSerAspLysThrLysGluHis......AspGlyGlnCysLysAspL 40

 149 AGTGCCACAAAGGAACCTACTTGIACAAGACTGTCTAGGCTTCTGGGCAG 198
       |||||| ||||||||||||||||| ||||| |||||||||||
  40 euCysGlnProGlySerArgTyrLeuThrSerHisCysThrAlaLeu...Glu 55

 199 GATACGACTGCAGGGAGTGGAGAGCTGTTCACGCTTCAAAAA...AGAAAA 248
       ||| ||||||||||||||||||| ||||||| |||||||| ||||||
  56 LysThrGlnCysHisProCysAspSerGlyPheSerAlaGln...ppAs 72

 249 CCACCTCAGACACTGCCTCAGGTGTTCCAAAGGCCGAAAAGAAATGGGTC 298
       :||| ||||| |||| ||:: ||||| :|||||||||||||||||||
  72 GArgGluIleArqCysHisGluGlnHisArgHisCysGluCysProAsnAlaGluIleL 89

 299 AGGTGGAGATCCTCGTTGGACAGTGGAACGGGACAGCGTGGTGGTGGGTGC 448
       ||||||||||||||||||| :| ||||||||||||||||||||||||
  89 euArgValLysGlyGluGlyThrAlaGluSerAspThrValCysThrCys 105

 349 AGGAAGAAAACGAGTACGGGATTATTGGAGTGAAAAACTTTCCAGGCTT 398
       ||||: ||||::: |

::::::::||| ||| |||||::::||
106 LysGluHisGln   HisCysThrSerLysAspCysGluAlaCysAl 120

399 CAATTGCAGGCCTCTGCCTCCAATGGG.. .ACCGTGCCACCTCCCTGCCAGG 445
    ::: :::: |||||: ||| ||| :::: | ::: ::
120 aGlnHisThrProCysIleProGlyPheGlyValMetGlnMetAlaThrG 137

446 AGAAGAGAACACCGTGTCC ACCTGCCATGCAGTTCTTTCCTAAGA 492
    ::|||||| |||||||||| ::::::| ||::: |: |||
137 luThrThrAspThrValCysHisProCysProValGlyPhePheSerAsn 153

493 GAAAAC   GAGTGTTCTGTAGTAAGTGTAAG .. AA 527
    ::|||| :::::::::||:|| ::::: ||
154 GluSerLeuPheCysLysCysTyrProTrpThrSerSerCysGluAspCy 170

528 AAGCCTGCAGCTGGACCAACGAAGTTGACCTAGCCCAGAATTGACAAGTTAAGG 577
    ::|||||||| ::: ||||
170 sAsnLeuGluValLeuGln   LysG 178

578 GCACTGAGGACTGA 591
    :::||||||
178 lyThrSerGlnThr 182

seq_name: pir2:A46484

seq_documentation_block:
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins,
J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas ant
A:Reference number: A46484; MUID:92148151
A:Accession: A46484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-327 <WAT>
A:Cross-references: GB-M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A:Experimental source: BAM3 macrophage cell line
A:Note: sequence extracted from NCBI backbone (NCBID:81544; NCBID:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposable element
A:Reference number: A47254; MUID:93186576
A:Accession: A47254
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Cross-references: GB-S56490; NID:g204505; PIDN:AAB25700.1; PID:g204506
A:Experimental source: MRL lpr/lpr
A:Note: sequence extracted from NCBI backbone (NCBID:126850; NCBID:126853; NCBID:126851
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:44-79/Domain: NGF receptor repeat homology <NGA>
F:81-124/Domain: NGF receptor repeat homology <NGA>

alignment_scores:
    Quality: 169.50   Length: 161
    Ratio: 2.093   Gaps: 6
Percent Similarity: 50.311   Percent Identity: 27.950

alignment_block:
US-09-525-998A-11 x A46484

Align seq 1/1 to: A46484 from: 1 to: 327

28 CTGTCCCAATGTCTGTCTGTGGTTGGGCGGAAATAGATGCCAGG 77
   : ||||||||||||||| :::::::::::: |: :||||||
7 ValLeuProLeuValLeuAlaGlySerGlnLeuArgValHisThrGlnGl 23

78 GGTT   ATTGGAGATAGTGTG 96

::::::|| ||| |||
23 yThrAsnSerIleSerGluSerLeuLeuLysLeuArgArgValHisGluT 40

97 ......TGTCCCAAGGAAAATATATCCACCTCAAAATAATCG 135
      ::: ||| ||| :::: | ||| ::||||||
40 kAspLysAsnCysSerGluGlyLeuTyr..........GlnGlyGlyPro 53

136 ATTTGTGTAAAATGGCAAAAGAAGTATTGTGTACAATGACTGTCC 185
    ::|||||| |||:: ||| :::||||||
54 PheCysCysGlnProCysGlnProCysLysLysValGluAspCysLysV 70

186 AAGCCCGGAAGAAGACTGAGGAGTGCAAGCCTCCTCA 235
    :::|||||| |: |||::: ||: ::: :::||
70 sMetAsnGlyGlyThrProThrCysAlaLysCysThrGlyGlyLysGluT 87

236 GCGCTGTACAAAACGACCAGA..CAGTGCCCGAGCCTCCCAAACGC 282
    :::|||||| :|||||||| ::: ||| :|| |||
87 yrMetAspLysAsnHisSerTyrAlaAspLysCysArgArgCysThrLeuCys 103

283 CGAAAGAAATGGTTAAGGAGATCTTTCTGTGACAGTGACGGGA 332
    :::|||| ||||| || ||: ::: | ::| |||
104 AspGlnGluHisGlyLeuGluValGluThrAspAsnCysThrLeuThrGlnAs 120

333 CACGTGTGTGTGTAAAGACAACAGTAAGGCATTATTGGAGTGAAA 382
    :::|||| |||||| |||||| ::: |||
120 nThrLysCysLysCysLysProGlyAspPheThrCysAsp......SerProG 135

383 ACCTTTTCCAGTGCTTCAATTGCAGCCTGCCCTGCCAAATGGCACCGTGCAC 432
    ::: | :|||||| ||| || ||||||| ||
135 lyCysGluHisCysValArgCysAlaSerCysGluHisGlyThrLeuGlu 151

433 CTCTCGTGCCAGGAGAAGACAGAACAACAGGTGTGC 465
    :::|||| |: |||||||||||||||||||||
152 ....ProCysThrAlaThrSerAsnThrAsnCys 161

seq_name: pir2:D72175

seq_documentation_block:
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jan-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, F.F.; Massung, R.F.; Lo
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola mi
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB-Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

alignment_scores:
    Quality: 166.50   Length: 172
    Ratio: 1.936   Gaps: 9
Percent Similarity: 50.000   Percent Identity: 26.744

alignment_block:
US-09-525-998A-11 x D72175

Align seq 1/1 to: D72175 from: 1 to: 349

97 TGTCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTGCTGTAC 146
   ||| |||||||||||||||||||||||||||||||||||||||
32 CysLysAspThrGluTyr..........LysArgHisAsnLeuCysCysGlc 45

147 CAAGTGCTACAAAGGACCTACTTGTTAGTAAATGACTGTCCGGGGGGGGGC 196
   ::|||| ||| ||| :::

```
 45 uSerCysProProGlyThrTyrAlaSerArgLeuCysAspSerLys...T  61
                :::::::           ::: :::
 44 uSerCysProProGlyThrTyrAlaSerArgLeuCysAspSerLys...T  60

197 AGGATACGGATGCAGGAGGTGGATGCAGCGGGTCGTTCACGTTCAGAA 246
       :::::::: ::: :::  ::  :::::::  ::  :::::::  :::::::::
197 AGGATACGGATTCAGGAGTGCAGACGGGTCGTTCACGTTCAGAA 246

 61 hrAsnThrGlnCysThrProCysGlySerGlyThrPheThrSerArgAsn  77
                :::::::  ::::  ::::::::::  :::::::::::::::
 60 hrAsnThrGlnCysThrProCysGlySerGlyThrPheThrSerArgAsn  76

247 AACCACCTCAGACACGCCTCAGCGCTCC...AAATGCCGAAAGGAAAT 293
    :::::::::  ::::::::::::  :::::::::  ::::::::::::
247 AACCACCTGAGACACGCCTCAGCGCTGC...AAATGCCGAAAGGAAAT 293

 78 AsnHisLeuProAlaCysLeuSerCysAsGlyArgCysAsnSer.....  92
    :::::::::::::  :::::::::::::::::::::::::
 77 AsnHisLeuProAlaCysLeuSerCysAsnGlyArgCysAsnSer.....  91

294 GGGTCAGGTGGAGATCTTGCTGCCACGTGGACGGGAAGACGGTGTGTG 343
    :::::::::::  ::::::::::  ::::::::  ::::::::::::
294 GGGTCAGGTGGATCTTGCTGCCACGTGGACGGGAAGACGGTGTGTG 343

 93 .AsnGlnValGluThrArgSerCysAsnThrThrHisAspArgIleCysG 109
     :::::::::::: :: :: :::::::::::: :::::::
 92 .AsnGlnValGluThrArgSerCysAsnThrThrHisAspArgIleCysG 108

344 GCTGCAAGAAAACAGTACGGCATTATTGGAGTGAAAACCTTTCCAG 393
    :: ::::::::::::::  ::::::::::::::::::::::::::::
344 GCTGCAAGAAAACAGTACGGCATTATTGGAGTGAAAACCTTTCCAG 393

109 luCysSerProGlyTyrTyr.................         115
    ::: ::::::::::::::::
108 luCysSerProGlyTyrTyr.................         114

394 TGCTTC..........AATTGCAGCCTCTGCCTCAAATGGGACCGT 428
    ::::::             ::::::::::::::::::::::::::::
394 TGCTTC..........AATTGCAGCCTCTGCCTCAAATGGGACCGT 428

116 CysLeuLeuLysSerGlyCysLysAlaCysValSerGlnThr..     131
    ::::::::::::::: :::: ::::::::::::::
115 CysLeuLeuLysSerGlyCysLysAlaCysValSerGlnThr..     130

429 GCACCTCTCGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAG 478
    :::::::::::  ::  ::::::::::::::::   ::::::::::::::::
429 GCACCTCTCGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAG 478

132 .................lysCysGlyIleG 136
                        ::: :::::::::
131 .................lysCysGlyIleG 145

479 GTTCTTTCTAAGAGAAAACGAGTGTGTCC 519
    ::: :::                          TGTAGTAAC 519
    :::  ::::::::
479 GTTCTTTCTAAGAGAAAACGAGTGTGTCC...........TGTAGTAAC 519

136 lyTyrGlyValSerGlyHisThrSerValGlyAspValIleCysSerPro 152
    ::::::::::::::::::::::::::::::::::::::::::::::::
135 lyTyrGlyValSerGlyHisThrSerValGlyAspValIleCysSerPro 151

520 AAGAAAACCTGGAGTGCACCAAGTTGTGCCT 554
    :::                          :::
520 ACCCCAGATTGAGAAT 570
       :::::::: :: :::
520 TGT 522

153 CysGlyPheGlyThrTyrSerSerThrValSerSerThrAspLysCysGl 169
        :::::: :::::: :::::::
152 Cys 152

169 uProValProAsnAsn 174
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alignment_scores:
        Quality:  164.00        Length:      151
        Ratio:      2.130        Gaps:          8
Percent Similarity:  50.993   Percent Identity:  27.815

alignment_block:
US-09-525-998A-11 x T28623

Align seq 1/1  to: T28623  from: 1  to: 348

 97 TGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTGCTGTAC 146
    ::  :::                    ::::::::::  :::::::::::
 31 CysLysAspThrGlnTyr.......LysArgHisAsnLeuCysLysLe  44

147 CAAGTGCACAAGGAACCTACTTGTACAAAGAACTGTGCACGCGGGGGC 196
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